

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
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Easton, Alan M.  
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Olins, Peter O.  
Paik, Kumnan  
Thomas, John W.
- (ii) TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
- (iii) NUMBER OF SEQUENCES: 197
- (iv) CORRESPONDENCE ADDRESS:  
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(C) CITY: St. Louis  
(D) STATE: Missouri  
(E) COUNTRY: USA  
(F) ZIP: 63167
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: not assigned  
(B) FILING DATE: 22-FEB-2002  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/762,227  
(B) FILING DATE: 09-DEC-1996
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/192,325  
(B) FILING DATE: 14-FEB-1994
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/446,872  
(B) FILING DATE: 06-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: S. Christopher Bauer  
(B) REGISTRATION NUMBER: 42,305  
(C) REFERENCE/DOCKET NUMBER: C-2790/6
- (ix) TELECOMMUNICATION INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,

Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser, or  
Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,  
Gly, Val, Arg, Ser, Phe, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,  
His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His,  
Thr, Phe, Gly, Arg, Ala, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 27
- (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu,  
Gly, Arg, Thr, Ser, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys,  
Arg, Leu, Gln, Gly, Pro, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,  
Asn, Leu, Pro, Arg, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,  
His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,  
Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,  
Val, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33
- (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,

Leu, Gln, Ala, Thr, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp, Leu, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu, Trp, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn, Cys, Arg, Leu, His, Met, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr, Ile, Met, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 43
- (D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu, Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 44  
(D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,  
Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala,  
or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 45  
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg,  
Ser, Ala, Ile, Glu, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 46  
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,  
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr,  
Ile, Val, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 47  
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,  
Gly, Val, Ser, Arg, Pro, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu,  
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met,  
Val, or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 49  
(D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
Arg, Ala, Gly, Pro, Asn, His, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,  
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His,  
Phe, Met, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 52  
(D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn,  
His, Arg, Leu, Gly, Ser, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 53  
(D) OTHER INFORMATION: /note= "Xaa at position 53 is

Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 54
- (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 57
- (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 58
- (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu, Ser, Asp, Arg, Gln, Val, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 59
- (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu, Tyr, His, Leu, Pro, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 60
- (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala, Ser, Pro, Tyr, Asn, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 61
- (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe, Asn, Glu, Pro, Lys, Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, His, Val, Arg, Pro, Thr, Asp, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63

- (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg, Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala, Asn, Pro, Ser, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val, Thr, Pro, His, Leu, Phe, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 67  
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 69  
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 70  
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 71  
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 72  
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73

- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 74  
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 75  
(D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 76  
(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 77  
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 78  
(D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 79  
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 80  
(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 81  
(D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 82  
(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site



- (B) LOCATION: 83  
(D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro, Ala, Thr, Trp, Arg, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 84  
(D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys, Glu, Gly, Arg, Met, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 85  
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu, Asn, Val, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 86  
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro, Cys, Arg, Ala, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 87  
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, Trp, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 88  
(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala, Lys, Arg, Val, or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 89  
(D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 90  
(D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 92  
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 93

- (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 94  
 (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 96  
 (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro, Lys, Tyr, Gly, Ile, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 97  
 (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile, Val, Lys, Ala, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 98  
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 99  
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 102  
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly, Leu, Glu, Lys, Ser, Tyr, or Pro"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 103  
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp,  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 104  
 (D) OTHER INFORMATION: /note= "Xaa at position 104 is  
 Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala,  
 Phe, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 105  
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is  
 Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile,  
 Asp, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 106  
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,  
 Ser, Ala, Lys, Thr, Ile, Gly, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 108  
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,  
 Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 109  
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,  
 Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 110  
 (D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys,  
 Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 111  
 (D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu,  
 Ile, Arg, Asp, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 112  
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,  
 Val, Gln, Tyr, Glu, His, Ser, or Phe"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 113  
 (D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe,  
 Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val,

or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 114
- (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr, Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 115
- (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 116
- (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 117
- (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr, Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 118
- (D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 119
- (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 123

(D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys  
1 5 10 15  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
85 90 95  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa  
100 105 110  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu  
115 120 125  
Ser Leu Ala Ile Phe  
130

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17

(D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met  
 or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note="Xaa at position 21 is Asp  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,  
 Ala, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,  
 Val, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 25  
 (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,  
 His, Gln, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 26  
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is His  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,  
 Asn, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,  
 Gly, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,  
 Asp, Gly, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,  
 Arg, Gln, Asn, Gly, Ala, or Glu"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
 Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note="Xaa at position 54 is Arg  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,  
 Thr, Val, Leu, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,  
 Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val,  
 or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 62  
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,  
 Pro, Thr, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg  
 or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala  
 or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val  
 or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys  
 or Arg"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 67  
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser  
 Phe or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
 Ile, Phe, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 69  
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,  
 Ala, Pro, Thr, Glu, Arg, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 71  
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,  
 Pro, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 72  
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,  
 Glu, Arg, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73  
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 76  
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,  
 Val, Ala, Asn, Glu, Pro, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile  
 or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is  
 Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 80  
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,  
 Gly, Glu, or Arg"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 82  
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,  
 Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile,  
 Met, Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 83  
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro  
 or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 85  
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu  
 or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87  
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 88  
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala  
 or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 91  
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala  
 or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 93  
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,  
 Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,  
 Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 96  
 (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro  
 or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 97  
 (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile  
 or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99
- (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 100
- (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 101
- (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 104
- (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 105
- (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 108
- (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Ala, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 112
- (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 114
- (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 115
- (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 116
- (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 117
- (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Ile	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Lys	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Xaa	Xaa	Xaa	Ile	Leu
			35				40						45		

Met	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Asn	Leu	Glu	Xaa	Phe	Xaa	Xaa	Xaa
50							55				60				
Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Ile	Glu	Xaa	Xaa	Leu	Xaa	Xaa
65					70					75				80	
Leu	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	Xaa	Xaa
			85						90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys	Leu	Xaa
			100						105					110	
Phe	Xaa	Xaa	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
			115						120				125		
Ser	Leu	Ala	Ile	Phe											
	130														

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note="Xaa at position 29 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 50  
(D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Asn, Ser, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Pro, Thr, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 55  
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 56  
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 62  
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 64  
(D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 65  
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 67  
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser or Phe"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 68  
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu or Phe"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 69  
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 76

- (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Asn, Pro, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Asn, Met, Arg, Ile, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 80  
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn, Gly, Glu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 82  
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87  
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 88  
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 91  
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 93  
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr, Asp, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His, Pro, Arg, Val, Gly, Asn, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 98



(D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Ala, Thr, Gln, Glu, Lys, Met, Ser, Tyr, Val, or Leu"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 99  
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile or Leu"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys or Arg"

(ix) FEATURE;  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, Thr, His, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 105  
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ser, Ile, or Asp"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 108  
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Ala, or Ser"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 109  
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 112  
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr or Gln"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 116  
 (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Val, Trp, Ala, His, Phe, Tyr, or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 117  
 (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 120  
 (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,

Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Pro, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Met	Ile	Asp	Glu	Xaa	Ile	Xaa	Xaa	Leu	Lys	Xaa	Xaa	Pro	Xaa
			20				25						30		
Pro	Xaa	Xaa	Asp	Phe	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa	Ile	Leu
			35				40					45			
Met	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Glu	Ala	Phe	Xaa	Arg	Xaa
			50				55				60				
Xaa	Lys	Xaa	Xaa	Xaa	Asn	Ala	Ser	Ala	Ile	Glu	Xaa	Xaa	Leu	Xaa	Xaa
65					70				75					80	
Leu	Xaa	Pro	Cys	Leu	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	Xaa	Pro
				85					90					95	
Ile	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Xaa	Xaa	Lys	Leu	Xaa
				100					105				110		
Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
			115				120						125		
Ser	Leu	Ala	Ile	Phe											
			130												

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 1  
 (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may  
 not precede the amino acid in position 1"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 3  
 (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser,  
 Lys, Gly, Asp, Met, Gln, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 4  
 (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn,  
 His, Leu, Ile, Phe, Arg, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 5  
 (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met,  
 Phe, Ile, Arg, Gly, Ala, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 6  
 (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile,  
 Cys, Gln, Glu, Arg, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 7  
 (D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp,  
 Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser,  
 or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 8  
 (D) OTHER INFORMATION: /note= "Xaa at position 8 is Glu,  
 Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val,  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 9  
 (D) OTHER INFORMATION: /note= "Xaa at position 9 is  
 Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile,  
 Gly, Val, Arg, Ser, Phe, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,  
 His, Gly, Gln, Arg, Pro, or Ala"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /note= "Xaa at position 12 is His,  
 Thr, Phe, Gly, Arg, Ala, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 13  
 (D) OTHER INFORMATION: /note= "Xaa at position 13 is Leu,  
 Gly, Arg, Thr, Ser, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 14  
 (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys,  
 Arg, Leu, Gln, Gly, Pro, Val, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 15  
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,  
 Asn, Leu, Pro, Arg, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 16  
 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,  
 His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 17  
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,  
 Asp, Gly, Ala, Arg, Leu, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,  
 Val, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 19  
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro,  
 Leu, Gln, Ala, Thr, or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,  
 Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,  
 Ile, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 21  
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,  
 Ala, Gly, Asn, Pro, Gln, or Val"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 22  
 (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp,  
 Leu, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,  
 Ser, Pro, Trp, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 26  
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is Leu,  
 Trp, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 27  
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,  
 Cys, Arg, Leu, His, Met, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,  
 Asp, Ser, Cys, Ala, Lys, Asn, Thr, Leu, Val, Glu,  
 Phe, Tyr, Ile, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Glu,  
 Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr,  
 Gly, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 30  
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp,  
 Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln,  
 Ala, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,  
 Pro, Phe, Val, Met, Leu, Thr, Lys, Asp, Asn, Arg,  
 Ser, Ala, Ile, Glu, His, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 32  
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,  
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala,  
Tyr, Ile, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 33  
(D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile,  
Gly, Val, Ser, Arg, Pro, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 34  
(D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,  
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala,  
Met, Val, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 35  
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,  
Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 36  
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,  
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val,  
His, Phe, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 37  
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,  
Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 38  
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,  
His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 39  
(D) OTHER INFORMATION: /note= "Xaa at position 39 is  
Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 40  
(D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg,  
Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His,  
Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 41  
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,  
Thr, Val, Ser, Leu, or Gly"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,  
 Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,  
 Phe, Leu, Val, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 43  
 (D) OTHER INFORMATION: /note= "Xaa at position 43 is Asn  
 or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 44  
 (D) OTHER INFORMATION: /note= "Xaa at position 44 is Leu,  
 Ser, Asp, Arg, Gln, Val, or Cys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 45  
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu,  
 Tyr, His, Leu, Pro, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala,  
 Ser, Pro, Tyr, Asn, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 47  
 (D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe,  
 Asn, Glu, Pro, Lys, Arg, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 48  
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,  
 His, Val, Arg, Pro, Thr, Asp, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 49  
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg,  
 Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala,  
 Asn, Pro, Ser, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val,  
 Thr, Pro, His, Leu, Phe, or Ser"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 52  
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 56  
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn, Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 57  
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 58  
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 59  
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 60  
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile, Met, Thr, Pro, Arg, Gly, Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 61  
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"



- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 62  
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 63  
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile, Ser, Arg, Thr, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 64  
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Leu, Ala, Ser, Glu, Phe, Gly, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 65  
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 66  
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn, Trp, Val, Gly, Thr, Leu, Glu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 67  
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu, Gln, Gly, Ala, Trp, Arg, Val, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 68  
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala, Tyr, Phe, Ile, Met, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 69  
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro, Ala, Thr, Trp, Arg, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 70  
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Cys, Glu, Gly, Arg, Met, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 71  
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu, Asn, Val, or Gln"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 72  
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Pro,  
 Cys, Arg, Ala, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 73  
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,  
 Ser, Trp, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 74  
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala,  
 Lys, Arg, Val, or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 75  
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr,  
 Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 76  
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala,  
 Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala,  
 Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 78  
 (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro,  
 Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,  
 Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 80  
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Arg,  
 Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,  
 Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser,  
 Ala, Trp, Phe, Ile, or Tyr"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 82  
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro,  
 Lys, Tyr, Gly, Ile, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 83  
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile,  
 Val, Lys, Ala, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 84  
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,  
 Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser,  
 Phe, Met, Val, Lys, Arg, Tyr, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 85  
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is  
 Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser,  
 Phe, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 86  
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is  
 Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87  
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is  
 Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn,  
 Ser, Ala, Gly, Ile, Leu, or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 88  
 (D) OTHER INFORMATION: /note= "Xaa at position 88 Gly,  
 Leu, Glu, Lys, Ser, Tyr, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 89  
 (D) OTHER INFORMATION: /note= "Xaa at position 89 is Asp  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 90  
 (D) OTHER INFORMATION: /note= "Xaa at position 90 is  
 Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys,  
 Ala, Phe, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is  
Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,  
Ile, Asp, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 92  
(D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu,  
Ser, Ala, Lys, Thr, Ile, Gly, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 94  
(D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,  
Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 95  
(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 96  
(D) OTHER INFORMATION: /note= "Xaa at position 96 is Lys,  
Asn, Thr, Leu, Gln, Arg, His, Glu, Ser, Ala,  
or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 97  
(D) OTHER INFORMATION: /note= "Xaa at position 97 is Leu,  
Ile, Arg, Asp, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 98  
(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,  
Val, Gln, Tyr, Glu, His, Ser, or Phe"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 99  
(D) OTHER INFORMATION: /note= "Xaa at position 99 is Phe,  
Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile,  
Val, or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 100  
(D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr,  
Cys, His, Ser, Trp, Arg, or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 101  
(D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu,  
Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 102
- (D) OTHER INFORMATION: /note= "Xaa at position 102 is  
Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp,  
Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 103
- (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,  
Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 104
- (D) OTHER INFORMATION: /note= "Xaa at position 104 is Leu,  
Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 105
- (D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu,  
Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
Ala, Pro, Leu, His, Val or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 107
- (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,  
Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 108
- (D) OTHER INFORMATION: /note= "Xaa at position 108 is  
Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,  
or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,  
Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				20				25						30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				35				40						45		

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
50						55						60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65						70					75					80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa
						85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln		
						100					105					110	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10

(D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile,  
Val, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 11

(D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,  
His, Gln, or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 12

(D) OTHER INFORMATION: /note= "Xaa at position 12 is His  
or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 15

(D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,  
Asn, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 16

(D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,  
Gly, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 17

(D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,  
Asp, Gly, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,  
Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 19

(D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro  
or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 20

(D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,  
Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe,  
Thr, or Met"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 21

(D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,  
Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 23

(D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,  
Ser, Pro, or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 24

(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn  
or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 28

(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,  
Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 30

(D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp  
or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 31

(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,  
Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 32

(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,  
Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys,  
Tyr, Val, or Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 36

(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,  
Ala, Asn, Ser, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 37

(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,  
Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 40

(D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg  
or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 41

(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,  
Thr, Val, Leu, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 42



- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val, or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 48  
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Pro, Thr, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 49  
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg or Lys"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51  
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 52  
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 53  
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Phe, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 54  
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu, Ile, Phe, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 55  
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Pro, Thr, Glu, Arg, or Gly"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 57

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(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,  
Pro, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 58

(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,  
Glu, Arg, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 59

(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala  
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 62

(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile  
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 65

(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
Thr, Gly, Asn, Met, Arg, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 66

(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
Gly, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 68

(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,  
Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 69

(D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro  
or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 71

(D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu  
or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 73

- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 74  
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 77  
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 79  
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 82  
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 83  
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 84  
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 85  
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, or Val"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 86  
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Arg, Ile, Gln, Pro, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87

(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 90  
 (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp or Leu"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 91  
 (D) OTHER INFORMATION: /note="Xaa at position 91 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 92  
 (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu or Gly"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 94  
 (C) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ala, or Ser"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 98  
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr, Val, or Gln"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 100  
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr or Trp"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 101  
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu or Ala"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 102  
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 103  
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr"

or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 107
- (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 108
- (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Cys	Xaa	Xaa	Xaa	Ile	Xaa	Glu	Xaa	Xaa	Xaa	Leu	Lys	Xaa	Xaa
1				5				10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Xaa	Xaa
				20				25				30		
Ile	Leu	Met	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Asn	Leu	Glu	Xaa	Phe
		35					40					45		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Ile	Glu	Xaa	Leu
		50					55				60			
Xaa	Xaa	Leu	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Arg
65					70					75				80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Lys
					85				90				95	
Leu	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln
					100				105				110	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 3  
(D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 4  
(D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 9  
(D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 15  
(D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 16  
(D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 18  
(D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Asn, or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 20  
(D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site

- (B) LOCATION: 21  
(D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 24  
(D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 28  
(D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 31  
(D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 32  
(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp, Phe, Ser, Ala, Gln, Glu, His, Val, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 36  
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Asn, Ser, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 37  
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Pro, Thr, or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 41  
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Leu, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 42  
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 48  
(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Pro, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 50

- (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala  
or Asn"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 51  
(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val  
or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 53  
(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser  
or Phe"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 54  
(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu  
or Phe"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 55  
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,  
Ala, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 62  
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
Val, Asn, Pro, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 63  
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 65  
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
Asn, Met, Arg, Ile, or Gly"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 66  
(D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,  
Gly, Glu, or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 68  
(D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser,  
Thr, Tyr, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 73



- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 74  
(D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala  
or Trp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 77  
(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala  
or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 79  
(D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,  
Asp, or Ala"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 81  
(D) OTHER INFORMATION: /note= "Xaa at position 81 is His,  
Pro, Arg, Val, Gly, Asn, Ser, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 84  
(D) OTHER INFORMATION: /note= "Xaa at position 84 is His,  
Ile, Asn, Leu, Ala, Thr, Arg, Gln, Glu, Lys, Met,  
Ser, Tyr, or Val"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 85  
(D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 86  
(D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys  
or Arg"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 87  
(D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,  
Pro, Met, Lys, His, Pro, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 91  
(D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn,  
Pro, Ser, Ile, or Asp"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 94

(D) OTHER INFORMATION: /note="Xaa at position 94 is Arg,  
Ala, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr  
or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 102

(D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,  
Val, Trp, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 103

(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,  
Ala, His, Phe, Tyr, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 106

(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 107

(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,  
Ser, Ile, Pro, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 108

(D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,  
Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,  
Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Cys Xaa Xaa Met Ile Asp Glu Xaa Ile Xaa Xaa Leu Lys Xaa Xaa  
1 5 10 15

Pro Xaa Pro Xaa Xaa Asp Phe Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa  
20 25 30

Ile Leu Met Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Glu Ala Phe Xaa

35	40	45
Arg Xaa Xaa Lys Xaa Xaa Xaa Asn Ala Ser Ala Ile Glu Xaa Xaa Leu		
50	55	60
Xaa Xaa Leu Xaa Pro Cys Leu Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg		
65	70	75
Xaa Pro Ile Xaa Xaa Xaa Xaa Gly Asp Trp Xaa Glu Phe Xaa Xaa Lys		
85	90	95
Leu Xaa Phe Tyr Leu Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln		
100	105	110

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 18
  - (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn or Ile"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 19
  - (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Ala, or Ile"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 20
  - (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Pro, or Leu"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 23
  - (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, or Leu"
- (ix) FEATURE:
  - (A) NAME/KEY: Modified-site
  - (B) LOCATION: 25
  - (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr or His"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 29  
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,  
 Arg, Val, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,  
 Ala, Asn, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 34  
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 37  
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,  
 Pro, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 38  
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 42  
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,  
 Ala, Ser, Asp, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 45  
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,  
 Val, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 46  
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 49  
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,  
 Ile, Leu, or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 50  
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu  
 or Asp"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 51

- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,  
Arg, or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 55  
(D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,  
Leu, or Thr"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 56  
(D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 59  
(D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu  
or Leu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 60  
(D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 62  
(D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn  
Val, or Pro"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 63  
(D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg  
or His"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 65  
(D) OTHER INFORMATION: /note= "Xaa at position 65 is Val  
or Ser"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 67  
(D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,  
Asn, His, or Gln"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 69  
(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln  
or Glu"
- (ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 73  
(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala

or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 76
- (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Ala, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu, Glu, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu, Ser, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 88
- (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 93
- (D) OTHER INFORMATION: /note= "Xaa at position 93 is Pro or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is His or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 100
- (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 101
- (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Ala, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 105
- (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg, Glu, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 112
- (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 116
- (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Val, Trp, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 117
- (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Gln, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Ser	Xaa	Xaa	Xaa	Asp	Glu	Xaa	Ile	Xaa	His	Leu	Lys	Xaa	Pro	Pro	Xaa
				20				25					30		





- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr  
 or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 15  
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,  
 Arg, Val, or Ile"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 18  
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,  
 Ala, Asn, or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 20  
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 23  
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,  
 Pro, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 24  
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn  
 or Ala"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 28  
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,  
 Ala, Ser, Asp, or Asn"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 31  
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,  
 Val, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 32  
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 35  
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,  
 Ile, or Asp"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu  
or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,  
Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,  
Leu, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro  
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu  
or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala  
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,  
Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 49
- (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg  
or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val  
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 53
- (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,  
Asn, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln"

or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 59
- (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala  
or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,  
Ala, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,  
Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,  
Glu, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,  
Glu, Val, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 71
- (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu  
or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73
- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,  
Ser, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 74
- (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala  
or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala  
or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Pro  
or Ser"

- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 81  
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His  
 or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 84  
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,  
 Ile, or Thr"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 86  
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys  
 or Arg"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 87  
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,  
 Ala, or Met"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 91  
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn  
 or Glu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 95  
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,  
 Glu, or Leu"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 98  
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr  
 or Gln"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 102  
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,  
 Val, Trp, or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 103  
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr  
 or Ser"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 106  
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,  
 Gln, or His"
- (ix) FEATURE:  
 (A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala  
or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Cys Ser Xaa Xaa Xaa Asp Glu Xaa Ile Xaa His Leu Lys Xaa Pro  
1 5 10 15  
Pro Xaa Pro Xaa Leu Asp Xaa Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa  
20 25 30  
Ile Leu Xaa Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Xaa Xaa Phe Xaa  
35 40 45  
Xaa Ala Xaa Lys Xaa Leu Xaa Asn Ala Ser Xaa Ile Glu Xaa Ile Leu  
50 55 60  
Xaa Asn Xaa Xaa Pro Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg  
65 70 75 80  
Xaa Pro Ile Xaa Ile Xaa Xaa Gly Asp Trp Xaa Glu Phe Arg Xaa Lys  
85 90 95  
Leu Xaa Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro  
1 5 10 15  
Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp  
20 25 30  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
35 40 45  
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu  
50 55 60  
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
65 70 75 80  
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys  
85 90 95  
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	
1				5					10					15		
Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	
			20					25					30			
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	
		35					40					45				
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	
	50					55					60					
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	
65					70					75					80	
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	
				85					90					95		
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln		
			100					105					110			

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Val	Pro	
1				5					10					15		
Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	
			20					25					30			
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	
		35					40					45				
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	
	50					55					60					
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	

65	70	75	80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys			
85	90	95	
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln			
100	105	110	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro			
1	5	10	15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp			
20	25	30	
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val			
35	40	45	
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu			
50	55	60	
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg			
65	70	75	80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys			
85	90	95	
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln			
100	105	110	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro			
1	5	10	15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp			
20	25	30	

Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
	50					55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
65					70					75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
	50					55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
65					70					75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105						110	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:



Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
		35					40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
	50					55					60				
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro  
1 5 10 15  
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp  
20 25 30  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
35 40 45  
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu  
50 55 60  
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
65 70 75 80  
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys  
85 90 95  
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro  
1 5 10 15  
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp  
20 25 30  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn  
35 40 45  
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu  
50 55 60  
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
65 70 75 80  
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys  
85 90 95  
Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1           5           10           15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
          20           25           30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
          50           55           60
Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65           70           75           80
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
          85           90           95
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
          100          105          110

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1           5           10           15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
          20           25           30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
          50           55           60

```

Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln	
				100				105						110	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro
1				5					10					15	
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp
			20					25					30		
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn
			35				40					45			
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu
			50			55					60				
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg
65					70					75					80
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln	Gln	
				100				105						110	

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5					10					15	
Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp
			20					25					30		

Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50				55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
		65			70					75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro
1				5				10						15	
Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp
			20					25					30		
Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	Phe	Val
		35					40					45			
Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu
		50				55					60				
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg
		65			70					75					80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys
				85					90					95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Val Pro  
1 5 10 15  
Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp Met Asp  
20 25 30  
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val  
35 40 45  
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu  
50 55 60  
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg  
65 70 75 80  
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys  
85 90 95  
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys  
1 5 10 15  
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp  
20 25 30  
Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala  
35 40 45  
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys
1				5					10					15	
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp
			20					25					30		
Gln	Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala
		35					40					45			
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				

Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser  
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro  
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg  
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:



Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
															Gln

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala

50		55		60											
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55				60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
20 25 30  
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp  
20 25 30  
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
			35				40					45			

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln  
 100 105 110  
 Gln

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
20 25 30  
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
20 25 30  
Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln

Gln

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110

Gln

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30



Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp  
20 25 30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
20 25 30  
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
20 25 30  
Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys  
1 5 10 15  
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Ala  
20 25 30  
Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp Ile Leu  
35 40 45  
Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val Arg Ala  
50 55 60  
Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn  
65 70 75 80  
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro  
85 90 95  
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr  
100 105 110  
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
115 120 125

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys  
1 5 10 15  
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn

20

25

30

Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu  
 35 40 45

Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala  
 50 55 60

Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn  
 65 70 75 80

Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro  
 85 90 95

Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr  
 100 105 110

Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys  
 1 5 10 15

Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp  
 20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110

Gln

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn  
1 5 10 15  
Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro  
20 25 30  
Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile  
35 40 45  
Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg  
50 55 60  
Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys  
65 70 75 80  
Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His  
85 90 95  
Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu  
100 105 110  
Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr  
115 120 125  
Leu Ser Leu Ala Ile Phe  
130

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly  
1 5 10 15  
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser  
20 25 30  
Gly Gly Gly Ser  
35

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Ser Pro Pro  
1                      5                      10                      15  
Ser Lys Glu Ser His Lys Ser Pro  
                    20

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Glu Gly Arg Ile Ser Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn  
1                      5                      10                      15  
Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
                    20                      25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 906 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATGGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC                      60  
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC                      120  
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA                      180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC                      240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT 360  
 TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC 420  
 TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT 480  
 GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG 540  
 GTGCTGCTCG GAACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG 600  
 GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG 660  
 CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CAACTGCAG 720  
 CTGGACGTCG CCGACTTTGC CACCACCATC TAACTGGGAA TGGCCCCTGC CCTGCAGCCC 780  
 ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 840  
 GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTCTACG CCACCTTGCG 900  
 CAGCCC 906

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT 360  
 TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT 420  
 GAAATTATAC ATCACTTAAA GAGACCACCT AACCTTTGC TGGACCCGAA CAACCTCAAT 480  
 TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC 540  
 GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC 600  
 CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA 660

GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	720
CAGGAACAAC AG	732

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 777 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCAC CGGCTCGTTC CCCGTCCCCG	420
TCTACCCAGC CGTGGGAACA CGTGAATGCC ATCCAGGAGG CCCGGCGTCT CCTGAACCTG	480
AGTAGAGACA CTGCTGCTGA GATGAATGAA ACAGTAGAAG TGATATCAGA AATGTTTGAC	540
CTCCAGGAGC CGACTTGCCT ACAGACCCGC CTGGAGCTGT ACAAGCAGGG CCTGCGGGGC	600
AGCCTCACCA AGCTCAAGGG CCCCTTGACC ATGATGGCCA GCCACTACAA GCAGCACTGC	660
CCTCCAACCC CGGAAACTTC CTGTGCAACC CAGATTATCA CCTTTGAAAG TTTCAAAGAG	720
AACCTGAAGG ACTTCCTGCT TGTATCCCC TTTGACTGCT GGGAGCCAGT CCAGGAG	777

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:



ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACTGCAG	720
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGAATGGCC	780
CCTGCCCTGC AGCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTC CAGTACCACC AGGTGAAGAT	420

TCCAAAGATG TGGCCGCCCC ACACAGACAG CCACTCACCT CTTCAGAACG AATTGACAAA	480
CAAATTCGGT ACATCCTCGA CGGGATATCA GCCCTGAGAA AGGAGACATG TAACAAGAGT	540
AACATGTGTG AAAGCAGCAA AGAGGCGCTA GCAGAAAACA ACCTGAACCT TCCAAAGATG	600
GCTGAAAAAG ATGGATGCTT CCAATCCGGA TTCAATGAGG AGACTTGCCT GGTGAAAATC	660
ATCACTGGTC TTTTGGAGTT TGAGGTATAC CTCGAGTACC TCCAGAACAG ATTTGAGAGT	720
AGTGAGGAAC AAGCCAGAGC TGTGCAGATG TCGACAAAAG TCCTGATCCA GTTCCTGCAG	780
AAAAAGGCAA AGAATCTAGA TGCAATAACC ACCCCTGACC CAACCACAAA TGCATCCCTG	840
CTGACGAAGC TGCAGGCACA GAACCAAGTGG CTGCAGGACA TGACAACTCA TCTCATTCTG	900
CGCAGCTTTA AGGAGTTCCT GCAGTCCAGC CTGAGGGCTC TTCGGCAAAT G	951

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT AACCTTTTGC TGGACCCGAA CAACCTCAAT	480
TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC	540
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	720
CAGGAACAAC AG	732

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 921 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 921 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
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CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360  
 TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC 420  
 TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT 480  
 GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG 540  
 GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG 600  
 GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG 660  
 CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGA CACACTGCAG 720  
 CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGAAGAAGT GGGAATGGCC 780  
 CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG 840  
 GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT 900  
 CTACGCCACC TTGCGCAGCC C 921

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
 CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
 CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360  
 TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT 420  
 GAAATTATAC ATCACTTAAA GAGACCACCT AACCCTTTGC TGGACCCGAA CAACCTCAAT 480

TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC	540
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	720
CAGGAACAAC AG	732

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT	540
ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTGTAAG GGCTGTCAAG	600
CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC	660
TCTGCCACGG CCGCACCCCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAGATT 360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420  
TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC 480  
TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT 540  
ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTCGTAAG GGCTGTCAAG 600  
CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC 660  
TCTGCCACGG CCGCACCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA 720  
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG 777

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420

TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTAACCC TTTGCTGGAC CCGAACAACC TCAATTCTGA AGACATGGAT	540
ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTGCTCG CATTCGTAAG GGCTGTCAAG	600
CACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC	660
TCTGCCACGG CCGCACCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCCGGGC CTCCTGTCAA TGCTGGCGGC GGCTCTGGTG GTGGTTCTGG TGGCGGCTCT	420
GAGGGTGGCG GCTCTGAGGG TGGCGTTCT GAGGGTGGCG GCTCTGAGGG TGGCGGTTCC	480
GGTGGCGGCT CCGGTTCCGG TGATTTTGAT TATGAAAACA TGGCTACACC ATTGGGCCCT	540
GCCAGCTCCC TGCCCCAGAG CTCCTGCTC AAGTCTTTAG AGCAAGTGAG GAAGATCCAG	600
GGCGATGGCG CAGCGCTCCA GGAGAAGCTG TGTGCCACCT ACAAGCTGTG CCACCCGAG	660
GAGCTGGTGC TGCTCGGACA CTCTCTGGGC ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC	720
AGCCAGGCCC TGCAGCTGGC AGGCTGCTTG AGCCAACTCC ATAGCGGCCT TTTCTCTAC	780
CAGGGGCTCC TGCAGGCCCT GGAAGGGATA TCCCCGAGT TGGGTCCCAC CTTGGACACA	840
CTGCAGCTGG ACGTCGCCGA CTTTGCCACC ACCATCTGGC AGCAGATGGA AGAACTGGGA	900
ATGGCCCCTG CCCTGCAGCC CACCCAGGGT GCCATGCCGG CCTTCGCCTC TGCTTTCCAG	960
CGCCGGGCAG GAGGGGTCCT GGTGCTAGC CATCTGCAGA GCTTCCTGGA GGTGTCGTAC	1020

CGCGTTCTAC GCCACCTTGC GCAGCCC

1047

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCCGGGC CTCCTGTCAA TGCTGGCGGC GGCTCTGGTG GTGGTTCTGG TGGCGGCTCT	420
GAGGGTGGCG GCTCTGAGGG TGGCGTTCT GAGGGTGGCG GCTCTGAGGG TGGCGGTTCC	480
GGTGGCGGCT CCGGTTCCGG TGATTTTGAT TATGAAACA TGGCACCGGC TCGTTCCCCG	540
TCCCCGTCTA CCCAGCCGTG GGAACACGTG AATGCCATCC AGGAGGCCCG GCGTCTCCTG	600
AACCTGAGTA GAGACACTGC TGCTGAGATG AATGAAACAG TAGAAGTGAT ATCAGAAATG	660
TTTGACCTCC AGGAGCCGAC TTGCCTACAG ACCCGCCTGG AGCTGTACAA GCAGGGCCTG	720
CGGGGCAGCC TCACCAAGCT CAAGGGCCCC TTGACCATGA TGGCCAGCCA CTACAAGCAG	780
CACTGCCCTC CAACCCCGGA AACTTCCTGT GCAACCCAGA TTATCACCTT TGAAAGTTTC	840
AAAGAGAACC TGAAGGACTT CCTGCTTGTC ATCCCCTTTG ACTGCTGGGA GCCAGTCCAG	900
GAG	903

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300  
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT 360  
TCCCCCGGTG GCGGCGGCTC TGGTGGTGGT TCTGGTGGCG GCTCTGAGGG TGGCGGCTCT 420  
GAGGGTGGCG GTTCTGAGGG TGGCGGCTCT GAGGGTGGCG GTTCCGGTGG CGGCTCCGGT 480  
TCCGGTAACA TGGCTACACC ATTAGGCCCT GCCAGCTCCC TGCCCCAGAG CTCCTGCTC 540  
AAGTGCTTAG AGCAAGTGAG GAAGATCCAG GGCGATGGCG CAGCGCTCCA GGAGAAGCTG 600  
TGTGCCACCT ACAAGCTGTG CCACCCCGAG GAGCTGGTGC TGCTCGGACA CTCTCTGGGC 660  
ATCCCCTGGG CTCCCCTGAG CTCCTGCCCC AGCCAGGCC TGCAGCTGGC AGGCTGCTTG 720  
AGCCAACTCC ATAGCGGCCT TTTCTCTAC CAGGGGCTCC TGCAGGCCCT GGAAGGGATA 780  
TCCCCGAGT TGGGTCCCAC CTTGGACACA CTGCAGCTGG ACGTCGCCGA CTTTGCCACC 840  
ACCATCTGGC AGCAGATGGA AGAACTGGGA ATGGCCCCTG CCCTGCAGCC CACCCAGGGT 900  
GCCATGCCGG CCTTCGCCTC TGCTTTCCAG CGCCGGGCAG GAGGGGTCCT GGTGTGCTAGC 960  
CATCTGCAGA GCTTCCTGGA GGTGTCGTAC CGCGTTCTAC GCCACCTTGC GCAGCCC 1017

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60  
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120  
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300

TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCACCGGCT CGTTCCCCGT CCCCCTCTAC CCAGCCGTGG	480
GAACACGTGA ATGCCATCCA GGAGGCCCCG CGTCTCCTGA ACCTGAGTAG AGACACTGCT	540
GCTGAGATGA ATGAAACAGT AGAAGTGATA TCAGAAATGT TTGACCTCCA GGAGCCGACT	600
TGCCTACAGA CCCGCCTGGA GCTGTACAAG CAGGGCCTGC GGGGCAGCCT CACCAAGCTC	660

AAGGGCCCCCT TGACCATGAT GGCCAGCCAC TACAAGCAGC ACTGCCCTCC AACCCCGGAA	720
ACTTCCTGTG CAACCCAGAT TATCACCTTT GAAAGTTTCA AAGAGAACCT GAAGGACTTC	780
CTGCTTGTC TCCCTTTGA CTGCTGGGAG CCAGTCCAGG AG	822

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 966 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAAAGATT	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCTCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 966 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAAGTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTACACCA TTAGGCCCTG CCAGCTCCCT GCCCCAGAGC	480
TTCCTGCTCA AGTGCTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG	540
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCGAGG AGCTGGTGCT GCTCGGACAC	600
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA	660
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG	720
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG	900
GTTGCTAGCC ATTCGCAGAG CTTCTGGAG GTGTCTGACC GCGTTCTACG CCACCTTGCG	960
CAGCCC	966

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 921 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
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GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTT CCCCGGGTGG TGGTTCTGGC GCGGCTCCA ACATGGCTAA CTGCTCTATA	600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTA ACCCTTTGCT GGACCCGAAC	660
AACCTCAATT CTGAAGACAT GGATATCCTG ATGGAACGAA ACCTTCGAAC TCCAAACCTG	720
CTCGCATTCG TAAGGGCTGT CAAGCACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT	780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC	840
ATCAAGGCAG GTGACTGGCA AGAATTCGG GAAAACTGA CGTTCTATCT GGTACCCCTT	900
GAGCAAGCGC AGGAACAACA G	921

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATGGCTACAC CATTAGGCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480

AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTT CCCCCGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	600
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT	660
ATACATCACT TAAAGAGACC ACCTAACCTT TTGCTGGACC CGAACAACCT CAATTCTGAA	720
GACATGGATA TCCTGATGGA ACGAAACCTT CGAACTCCAA ACCTGCTCGC ATTCGTAAGG	780
GCTGTCAAGC ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA	840
TGTCTGCCCT CTGCCACGGC CGCACCTCTT CGACATCCAA TCATCATCAA GGCAGGTGAC	900
TGGCAAGAAT TCCGGGAAAA ACTGACGTTT TATCTGGTTA CCCTTGAGCA AGCGCAGGAA	960
CAACAG	966

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1047 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTT CCCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT	600
GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT	660
GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTTGATT ATGAAAACAT GGCTAACTGC	720
TCTATAATGA TCGATGAAAT TATACATCAC TTAAAGAGAC CACCTAACCC TTTGCTGGAC	780
CCGAACAACC TCAATTCTGA AGACATGGAT ATCCTGATGG AACGAAACCT TCGAACTCCA	840

AACCTGCTCG CATTCTGTAAG GGCTGTCAAG CACTTAGAAA ATGCATCAGG TATTGAGGCA	900
ATTCTTCGTA ATCTCCAACC ATGTCTGCCC TCTGCCACGG CCGCACCTC TCGACATCCA	960
ATCATCATCA AGGCAGGTGA CTGGCAAGAA TTCCGGGAAA AACTGACGTT CTATCTGGTT	1020
ACCCTTGAGC AAGCGCAGGA ACAACAG	1047

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CTTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTT CCCCGGGTGG TGGTTCTGGC GGGCGCTCCA ACATGGCTAA CTGCTCTATA	600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC	660
AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG	720
GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT	780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC	840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA CGTTCTATCT GGTACCTT	900
GAGCAAGCGC AGGAACAACA G	921

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1047 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATGGCTACAC	CATTAGGCCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTGCTTA	60
GAGCAAGTGA	GGAAGATCCA	GGGCGATGGC	GCAGCGCTCC	AGGAGAAGCT	GTGTGCCACC	120
TACAAGCTGT	GCCACCCCGA	GGAGCTGGTG	CTGCTCGGAC	ACTCTCTGGG	CATCCCCTGG	180
GCTCCCCTGA	GCTCCTGCCC	CAGCCAGGCC	CTGCAGCTGG	CAGGCTGCTT	GAGCCAACTC	240
CATAGCGGCC	TTTTCTCTA	CCAGGGGCTC	CTGCAGGCC	TGGAAGGGAT	ATCCCCCGAG	300
TTGGGTCCCA	CCTTGGACAC	ACTGCAGCTG	GACGTCGCCG	ACTTTGCCAC	CACCATCTGG	360
CAGCAGATGG	AAGAACTGGG	AATGGCCCCCT	GCCCTGCAGC	CCACCCAGGG	TGCCATGCCG	420
GCCTTCGCCT	CTGCTTTCCA	GCGCCGGGCA	GGAGGGGTCC	TGGTTGCTAG	CCATCTGCAG	480
AGCTTCCTGG	AGGTGTCGTA	CCGCGTTCTA	CGCCACCTTG	CGCAGCCCTA	CGTAATCGAG	540
GGAAGGATTT	CCCCCGGGCC	TCCTGTCAAT	GCTGGCGGCG	GCTCTGGTGG	TGGTTCGGT	600
GGCGGCTCTG	AGGGTGGCGG	CTCTGAGGGT	GGCGGTTCTG	AGGGTGGCGG	CTCTGAGGGT	660
GGCGGTTCCG	GTGGCGGCTC	CGGTTCCGGT	GATTTTGATT	ATGAAAACAT	GGCTAACTGC	720
TCTATAATGA	TCGATGAAAT	TATACATCAC	TTAAAGAGAC	CACCTGCACC	TTTGCTGGAC	780
CCGAACAACC	TCAATGACGA	AGACGTCTCT	ATCCTGATGG	AACGAAACCT	TCGACTTCCA	840
AACCTGGAGA	GCTTCGTAAG	GGCTGTCAAG	AACCTAGAAA	ATGCATCAGG	TATTGAGGCA	900
ATTCTTCGTA	ATCTCCAACC	ATGTCTGCCC	TCTGCCACGG	CCGCACCCTC	TCGACATCCA	960
ATCATCATCA	AGGCAGGTGA	CTGGCAAGAA	TTCCGGGAAA	AACTGACGTT	CTATCTGGTT	1020
ACCCTTGAGC	AAGCGCAGGA	ACAACAG				1047

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATGGCTACAC	CATTAGGCCC	TGCCAGCTCC	CTGCCCCAGA	GCTTCCTGCT	CAAGTGCTTA	60
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GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAATCGAG	540
GGAAGGATTT CCCCggGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	600
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT	660
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA	720
GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG	780
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA	840
TGTCTGCCCT CTGCCACGGC CGCACCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC	900
TGGCAAGAAT TCCGGGAAAA ACTGACGTTT TATCTGGTTA CCCTTGAGCA AGCGCAGGAA	960
CAACAG	966

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATGGCTACAC CATTAGGCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420

GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC	540
GGTGGAGGCT CCCCGGGTGG TGGTTCTGGC GCGGGCTCCA ACATGGCTAA CTGCTCTATA	600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC	660
AACCTCAATG ACGAAGACGT CTCTATCCTG ATGGAACGAA ACCTTCGACT TCCAAACCTG	720
GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT	780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC	840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA CGTTCTATCT GGTTACCCTT	900
GAGCAAGCGC AGGAACAACA G	921

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATGGCTACAC CATTAGGCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC	540
GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG	600
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT	660
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA	720
GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG	780
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA	840

TGTCTGCCCT CTGCCACGGC CGCACCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC	900
TGGCAAGAAT TCCGGGAAAA ACTGACGTTT TATCTGGTTA CCCTTGAGCA AGCGCAGGAA	960
CAACAG	966

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC	540
GGTGGAGGCT CCCCAGGTGG TGGTTCTGGC GGCGGCTCCA ACATGGCTAA CTGCTCTATA	600
ATGATCGATG AAATTATACA TCACTTAAAG AGACCACCTG CACCTTTGCT GGACCCGAAC	660
AACCTCAATG ACGAAGACGT CTCTATCTTG ATGGAACGAA ACCTTCGACT TCCAAACCTG	720
GAGAGCTTCG TAAGGGCTGT CAAGAACTTA GAAAATGCAT CAGGTATTGA GGCAATTCTT	780
CGTAATCTCC AACCATGTCT GCCCTCTGCC ACGGCCGCAC CCTCTCGACA TCCAATCATC	840
ATCAAGGCAG GTGACTGGCA AGAATTCCGG GAAAACTGA CGTTCTATCT GGTACCCTT	900
GAGCAAGCGC AGGAACAACA G	921

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 966 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA 60  
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC 120  
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG 180  
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC 240  
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG 300  
TTGGGTCCCA CTTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG 360  
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG 420  
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG 480  
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTA CGTAGAGGGC 540  
GGTGGAGGCT CCCCGGGTGA ACCGTCTGGT CCAATCTCTA CTATCAACCC GTCTCCTCCG 600  
TCTAAAGAAT CTCATAAATC TCCAAACATG GCTAACTGCT CTATAATGAT CGATGAAATT 660  
ATACATCACT TAAAGAGACC ACCTGCACCT TTGCTGGACC CGAACAACCT CAATGACGAA 720  
GACGTCTCTA TCCTGATGGA ACGAAACCTT CGACTTCCAA ACCTGGAGAG CTTCGTAAGG 780  
GCTGTCAAGA ACTTAGAAAA TGCATCAGGT ATTGAGGCAA TTCTTCGTAA TCTCCAACCA 840  
TGTCTGCCCT CTGCCACGGC CGCACCTCT CGACATCCAA TCATCATCAA GGCAGGTGAC 900  
TGGCAAGAAT TCCGGGAAAA ACTGACGTTT TATCTGGTTA CCCTTGAGCA AGCGCAGGAA 960  
CAACAG 966

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120

CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAAGTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAGT	ACGTAATCGA	GGGAAGGATT	360
TCCCCGGGTG	AACCGTCTGG	TCCAATCTCT	ACTATCAACC	CGTCTCCTCC	GTCTAAAGAA	420
TCTCATAAAT	CTCCAAACAT	GGCTAACTGC	TCTATAATGA	TCGATGAAAT	TATACATCAC	480
TTAAAGAGAC	CACCTGCACC	TTTGCTGGAC	CCGAACAACC	TCAATGACGA	AGACGTCTCT	540
ATCCTGATGG	AACGAAACCT	TCGACTTCCA	AACCTGGAGA	GCTTCGTAAG	GGCTGTCAAG	600
AACTTAGAAA	ATGCATCAGG	TATTGAGGCA	ATTCTTCGTA	ATCTCCAACC	ATGTCTGCCC	660
TCTGCCACGG	CCGCACCCTC	TCGACATCCA	ATCATCATCA	AGGCAGGTGA	CTGGCAAGAA	720
TTCCGGGAAA	AACTGACGTT	CTATCTGGTT	ACCCTTGAGC	AAGCGCAGGA	ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTGCA	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATGAC	GAAGACGTCT	CTATCCTGAT	GGAACGAAAC	120
CTTCGACTTC	CAAACCTGGA	GAGCTTCGTA	AGGGCTGTCA	AGAACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAAGTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAGT	ACGTAATCGA	GGGAAGGATT	360
TCCCCGGGTG	AACCGTCTGG	TCCAATCTCT	ACTATCAACC	CGTCTCCTCC	GTCTAAAGAA	420
TCTCATAAAT	CTCCAAACAT	GGCTACACCA	TTGGGCCCTG	CCAGCTCCCT	GCCCCAGAGC	480
TTCCTGCTCA	AGTCTTTAGA	GCAAGTGAGG	AAGATCCAGG	GCGATGGCGC	AGCGCTCCAG	540
GAGAAGCTGT	GTGCCACCTA	CAAGCTGTGC	CACCCCGAGG	AGCTGGTGCT	GCTCGGACAC	600
TCTCTGGGCA	TCCCCTGGGC	TCCCCTGAGC	TCCTGCCCCA	GCCAGGCCCT	GCAGCTGGCA	660
GGCTGCTTGA	GCCAACTCCA	TAGCGGCCTT	TTCCTCTACC	AGGGGCTCCT	GCAGGCCCTG	720

GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC	780
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCTGC CCTGCAGCCC	840
ACCCAGGGTG CCATGCCGGC CTTGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG	900
GTTGCTAGCC ATCTGCAGAG CTTCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG	960
CAGCCCTGAT AAGGATCCGA ATTC	984

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTAGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTGC TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG	720
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGA CACACTGCAG	720
CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGAATGGCC	780
CCTGCCCTGC AGCCCACCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 732 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120

CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT	480
GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC	540
GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	720
CAGGAACAAC AG	732

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA CACCATTGGG CCCTGCCAGC	420
TCCCTGCCCC AGAGCTTCCT GCTCAAGTCT TTAGAGCAAG TGAGGAAGAT CCAGGGCGAT	480
GGCGCAGCGC TCCAGGAGAA GCTGTGTGCC ACCTACAAGC TGTGCCACCC CGAGGAGCTG	540
GTGCTGCTCG GACACTCTCT GGGCATCCCC TGGGCTCCCC TGAGCTCCTG CCCCAGCCAG	600
GCCCTGCAGC TGGCAGGCTG CTTGAGCCAA CTCCATAGCG GCCTTTTCCT CTACCAGGGG	660
CTCCTGCAGG CCCTGGAAGG GATATCCCCC GAGTTGGGTC CCACCTTGGA CACACTGCAG	720



CTGGACGTCG CCGACTTTGC CACCACCATC TGGCAGCAGA TGGAAGAACT GGGAAATGGCC	780
CCTGCCCTGC AGCCCACCCA GGGTGCCATG CCGGCCTTCG CCTCTGCTTT CCAGCGCCGG	840
GCAGGAGGGG TCCTGGTTGC TAGCCATCTG CAGAGCTTCC TGGAGGTGTC GTACCGCGTT	900
CTACGCCACC TTGCGCAGCC C	921

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	420
GAAATTATAC ATCACTTAAA GAGACCACCT GCACCTTTGC TGGACCCGAA CAACCTCAAT	480
GACGAAGACG TCTCTATCCT GATGGAACGA AACCTTCGAC TTCCAAACCT GGAGAGCTTC	540
GTAAGGGCTG TCAAGAACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	600
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	660
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	720
CAGGAACAAC AG	732

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240  
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300  
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC 360  
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA 420  
TCTCATAAAT CTCCAAACAT GGCTACACCA TTGGGCCCTG CCAGCTCCCT GCCCCAGAGC 480  
TTCCTGCTCA AGTCTTTAGA GCAAGTGAGG AAGATCCAGG GCGATGGCGC AGCGCTCCAG 540  
GAGAAGCTGT GTGCCACCTA CAAGCTGTGC CACCCCAGAG AGCTGGTGCT GCTCGGACAC 600  
TCTCTGGGCA TCCCCTGGGC TCCCCTGAGC TCCTGCCCCA GCCAGGCCCT GCAGCTGGCA 660  
GGCTGCTTGA GCCAACTCCA TAGCGGCCTT TTCCTCTACC AGGGGCTCCT GCAGGCCCTG 720  
GAAGGGATAT CCCCCGAGTT GGGTCCCACC TTGGACACAC TGCAGCTGGA CGTCGCCGAC 780  
TTTGCCACCA CCATCTGGCA GCAGATGGAA GAACTGGGAA TGGCCCCCTGC CCTGCAGCCC 840  
ACCCAGGGTG CCATGCCGGC CTTCGCCTCT GCTTTCCAGC GCCGGGCAGG AGGGGTCCTG 900  
GTTGCTAGCC ATCTGCAGAG CTTCCTGGAG GTGTCGTACC GCGTTCTACG CCACCTTGCG 960  
CAGCCC 966

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60  
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120  
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180  
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG AACCGTCTGG TCCAATCTCT ACTATCAACC CGTCTCCTCC GTCTAAAGAA	420
TCTCATAAAT CTCCAAACAT GGCTAACTGC TCTATAATGA TCGATGAAAT TATACATCAC	480
TTAAAGAGAC CACCTGCACC TTTGCTGGAC CCGAACAACC TCAATGACGA AGACGTCTCT	540
ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTGGAGA GCTTCGTAAG GGCTGTCAAG	600
AACTTAGAAA ATGCATCAGG TATTGAGGCA ATTCTTCGTA ATCTCCAACC ATGTCTGCCC	660
TCTGCCACGG CCGCACCTC TCGACATCCA ATCATCATCA AGGCAGGTGA CTGGCAAGAA	720
TTCCGGGAAA AACTGACGTT CTATCTGGTT ACCCTTGAGC AAGCGCAGGA ACAACAG	777

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AATTCCGGGA AAAACTGACG TTCTATCTGG TTACCCTTGA G	41
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(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGCGCTTGC TCAAGGGTAA CCAGATAGAA CGTCAGTTTT TCCCGG	46
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(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CAAGCGCAGG AACACAGTA CGTAATCGAG GGAAGGATT

39

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ACCCGGGGAA ATCCTTCCCT CGATTACGTA CTGTTGTTC

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGTAAG GTACCGCATG CAAGCTTAGA

60

TCT

63

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AGCTAGATCT AAGCTTGCAT GCGGTACCTT ACATGTTGGA GCCGCCGCCA GAACCACC 58

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCGGGTGAAC CGTCTGGTCC AATCTCTACT ATCAACCCGT CTCCTCCGTC TAAAGAATCT 60

CATAAATCTC CAAA 74

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGTTTGA GATTTATGAG ATTCTTTAGA CGGAGGAGAC GGGTTGATAG TAGAGATTGG 60

ACCAGACGGT TCAC 74

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTAGCCATCT GCAGAGCTTC CTGGAGGTGT CGTACCGCGT TCTACGCCAC CTTGCGCAGC 60  
CCTACGTA 68

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

AGCTTACGTA GGGCTGCGCA AGGTGGCGTA GAACGCGGTA CGACACCTCC AGGAAGCTCT 60  
GCAGATGG 68

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GTAATCGAGG GAAAGATTTC C 21

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCGGGGAAAT CTTTCCCTCG ATTAC 25

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GTAGAGGGCG GTGGAGGCTC C

21

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CCGGGGAGCC TCCACGCCC TCTAC

25

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "sythetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CATGGCACCA GCAAGATCAC CATCACCATC AACTCAACCT TGGGAACATG TGAATGCC

58

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATTCACATG TTCCCAAGGT TGAGTTGATG GTGATGGTGA TCTTGCTGGT GC 52

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGCCAGCTC CCTGCCCCAG AGCTTCCTGC TCAAGTCTTT AGAGCAAGTG AGGAAGATCC 60

AGGGCG 66

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGGATCTTC CTCACTTGCT CTAAAGACTT GAGCAGGAAG CTCTGGGGCA GGGAGCTGGC 60

AGGGCC 66

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AGCTTACCTG CCATGGCTCC AGTACCACCA GGTGAAGATT CCAAAGAT

48

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TTGGAATCTT CACCTGGTGG TACTGGAGCC ATGGCAGGTA

40

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCTTCCATG GCTACCCCCC TGGGCC

26

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAGGGGGGTA GCCATGGA

18

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CATGGCTACA CCATTGGGCC

20

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAATGGTGTA GC

12

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CATGGCTACA CCATTAGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

TAATGGTGTA GC

12

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CCTGTCAACC CGGGCGGCGG CTCTGGTGGT

30

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TCATAATACA TGTTACCGGA ACGGAGCCGC C

31

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATCGTCTGAC CTCCCGGGAC CTCCTGTCAA TGCT

34

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AGCGTTTGAC ATGTTTTTCAT AATCAAAATC

30

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln	Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly
		115					120					125			

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
 130 135 140  
 Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
 145 150 155 160  
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
 165 170 175  
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
 180 185 190  
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
 195 200 205  
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
 210 215 220  
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 225 230 235 240  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 245 250 255  
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
 260 265 270  
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
 275 280 285  
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
 290 295 300  
 Ala Gln Pro  
 305

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
115 120 125  
Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
130 135 140  
Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
145 150 155 160  
Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
165 170 175  
Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
180 185 190  
Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
195 200 205  
Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
210 215 220  
Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
225 230 235 240  
Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
245 250 255  
Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
260 265 270  
Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
275 280 285  
His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
290 295 300  
Ala Gln Pro  
305

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly  
115 120 125

Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
130 135 140

Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
145 150 155 160

Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
165 170 175

Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
180 185 190

Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
195 200 205

Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
210 215 220

Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
225 230 235 240

Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
245 250 255

Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
260 265 270

Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
275 280 285

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
290 295 300

Ala Gln Pro  
305

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 307 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	
1				5					10					15		
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	
			20					25					30			
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	
		35					40					45				
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	
	50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	
65				70						75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
			85						90					95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	
			100					105					110			
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	
		115					120					125				
Gly	Ser	Asn	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	
		130				135					140					
Ser	Phe	Leu	Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	
145				150						155					160	
Gly	Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	
			165						170					175		
Pro	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	
			180					185					190			
Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	
		195					200					205				
Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	
	210					215					220					



Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 225 230 235 240  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 245 250 255  
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
 260 265 270  
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
 275 280 285  
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
 290 295 300  
 Ala Gln Pro  
 305

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His  
 130 135 140  
 His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn

145                      150                      155                      160  
 Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn  
                                  165                      170                      175  
 Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly  
                                  180                      185                      190  
 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr  
                                  195                      200                      205  
 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln  
                                  210                      215                      220  
 Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala  
                                  225                      230                      235                      240  
 Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1                      5                      10                      15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
                                  20                      25                      30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
                                  35                      40                      45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
                                  50                      55                      60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65                      70                      75                      80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
                                  85                      90                      95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
                                  100                      105                      110  
 Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly  
                                  115                      120                      125  
 Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His  
                                  130                      135                      140

His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn  
 145 150 155 160  
 Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn  
 165 170 175  
 Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly  
 180 185 190  
 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr  
 195 200 205  
 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln  
 210 215 220  
 Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala  
 225 230 235 240  
 Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125

Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His  
 130 135 140  
 His Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn  
 145 150 155 160  
 Ser Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn  
 165 170 175  
 Leu Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly  
 180 185 190  
 Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr  
 195 200 205  
 Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln  
 210 215 220  
 Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala  
 225 230 235 240  
 Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro

115					120					125					
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
130						135					140				
Pro	Asn	Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser
145					150					155					160
Phe	Leu	Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly
				165					170					175	
Ala	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro
			180					185					190		
Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro
		195					200					205			
Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser
	210					215					220				
Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu
225					230					235					240
Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu
				245					250					255	
Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu
			260					265					270		
Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe
		275					280					285			
Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His
	290					295					300				
Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala
305					310					315					320
Gln	Pro														

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro
          115          120          125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
          130          135          140

Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser
          145          150          155          160

Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly
          165          170          175

Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro
          180          185          190

Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro
          195          200          205

Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
          210          215          220

Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu
          225          230          235          240

Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu
          245          250          255

Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu
  
```

260	265	270
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe		
275	280	285
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His		
290	295	300
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala		
305	310	315
320		
Gln Pro		

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55				60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
		100						105					110		
Gln	Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro
		115					120					125			
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser
		130				135					140				
Pro	Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His
145					150					155					160
Leu	Lys	Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser
				165					170					175	



Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu  
 180 185 190  
 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile  
 195 200 205  
 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala  
 210 215 220  
 Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu  
 225 230 235 240  
 Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln  
 245 250 255  
 Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His  
 145 150 155 160  
 Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser  
 165 170 175  
 Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu  
 180 185 190  
 Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile  
 195 200 205  
 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala  
 210 215 220  
 Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu  
 225 230 235 240  
 Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln  
 245 250 255  
 Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30  
 Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro

115	120	125
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser 130 135 140		
Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His 145 150 155 160		
Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser 165 170 175		
Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu 180 185 190		
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile 195 200 205		
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala 210 215 220		
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu 225 230 235 240		
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln 245 250 255		
Glu Gln Gln		

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys 1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp 20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser 35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala 50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro 65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg 85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
 130 135 140  
 Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
 145 150 155 160  
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
 165 170 175  
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
 180 185 190  
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
 195 200 205  
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
 210 215 220  
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 225 230 235 240  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 245 250 255  
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
 260 265 270  
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
 275 280 285  
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
 290 295 300  
 Ala Gln Pro  
 305

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
 130 135 140  
 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
 145 150 155 160  
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
 165 170 175  
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
 180 185 190  
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
 195 200 205  
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
 210 215 220  
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 225 230 235 240  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 245 250 255  
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
 260 265 270  
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
 275 280 285  
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
 290 295 300  
 Ala Gln Pro  
 305

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
20 25 30  
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
115 120 125  
Gly Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His  
130 135 140  
His Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn  
145 150 155 160  
Asp Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn  
165 170 175  
Leu Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly  
180 185 190  
Ile Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr  
195 200 205  
Ala Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln  
210 215 220  
Glu Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala  
225 230 235 240  
Gln Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
          20           25           30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
          35           40           45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro
          115          120          125

Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser
          130          135          140

Pro Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His
145          150          155          160

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp
          165          170          175

Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu
          180          185          190

Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile
          195          200          205

Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala
          210          215          220

Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu
225          230          235          240

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln
          245          250          255
  
```

Glu Gln Gln

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
20 25 30  
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro  
115 120 125  
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
130 135 140  
Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser  
145 150 155 160  
Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly  
165 170 175  
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro  
180 185 190  
Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro  
195 200 205  
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
210 215 220  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu



225		230		235		240
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu						
		245		250		255
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu						
		260		265		270
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe						
		275		280		285
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His						
		290		295		300
Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala						
305		310		315		320
Gln Pro						

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys																			
1				5				10											15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp																			
			20					25											30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala																			
			35				40						45						
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala																			
			50				55						60						
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro																			
65					70				75										80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg																			
				85				90											95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln																			
			100					105											110
Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala																			
			115					120											125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly																			
			130				135												140

Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	145	150	155	160
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Asn	Met	Ala	Thr	165	170	175	
Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	Ser	180	185	190	
Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	Gln	Glu	195	200	205	
Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Val	Leu	210	215	220	
Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	Ser	Cys	Pro	225	230	235	240
Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	His	Ser	Gly	245	250	255	
Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	260	265	270	
Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	275	280	285	
Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	290	295	300	
Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	305	310	315	320
Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	325	330	335	
Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro				340	345		

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGATCCACCA TGAGCCGCCT GCCCGTCCTG CTCCTGCTCC AACTCCTGGT CCGCCCCGCC	60
ATGG	64

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	
1				5					10					15		
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	
			20					25					30			
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	
		35					40					45				
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	
	50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	
65					70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	
				85					90					95		
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	
			100					105					110			
Gln	Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	
		115					120					125				
Gly	Ser	Asn	Met	Ala	Pro	Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro	
		130				135					140					
Trp	Glu	His	Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu	
145					150					155					160	
Ser	Arg	Asp	Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	
				165					170					175		
Glu	Met	Phe	Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	
			180					185					190			
Leu	Tyr	Lys	Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	
		195					200					205				
Leu	Thr	Met	Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	
	210					215					220					
Glu	Thr	Ser	Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	
225					230					235					240	
Asn	Leu	Lys	Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	
				245					250					255		

Val Gln Glu

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 301 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70						75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln	Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gln	Pro	Pro	Val	Asn	Ala
	115						120					125			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly
	130					135					140				
Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser
145					150					155					160
Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Asn	Met	Ala	Pro
			165					170						175	
Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro	Trp	Glu	His	Val	Asn	Ala
			180					185					190		
Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu	Ser	Arg	Asp	Thr	Ala	Ala
	195					200						205			
Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe	Asp	Leu	Gln
	210					215					220				

Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys	Gln	Gly	Leu	225	230	235	240
Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met	Met	Ala	Ser	245	250	255	
His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser	Cys	Ala	Thr	260	265	270	
Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys	Asp	Phe	Leu	275	280	285	
Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu				290	295	300	

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	20	25	30	
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Pro	Val	Asn	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	130	135	140	
Gly	Ser	Glu	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asn	Met	145	150	155	160
Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu				

175

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
325 330 335

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro  
 115 120 125  
 Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
 130 135 140  
 Pro Asn Met Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp  
 145 150 155 160  
 Glu His Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser  
 165 170 175  
 Arg Asp Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu  
 180 185 190  
 Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu  
 195 200 205  
 Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu  
 210 215 220  
 Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu  
 225 230 235 240  
 Thr Ser Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn  
 245 250 255  
 Leu Lys Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val  
 260 265 270  
 Gln Glu

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
 20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
 35 40 45  
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60  
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Gly Ser Asn Met Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val  
 130 135 140  
 Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys  
 145 150 155 160  
 Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr  
 165 170 175  
 Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu  
 180 185 190  
 Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln  
 195 200 205  
 Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu  
 210 215 220  
 Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser  
 225 230 235 240  
 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile  
 245 250 255  
 Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro  
 260 265 270  
 Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn  
 275 280 285  
 Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys  
 290 295 300  
 Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 307 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu  
1 5 10 15  
Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala  
20 25 30  
Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu  
35 40 45  
Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser  
50 55 60  
Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu  
65 70 75 80  
His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly  
85 90 95  
Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val  
100 105 110  
Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met  
115 120 125  
Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser  
130 135 140  
Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln  
145 150 155 160  
Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
165 170 175  
Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly  
180 185 190  
Ser Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His  
195 200 205  
Leu Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser  
210 215 220  
Glu Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu  
225 230 235 240  
Leu Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile  
245 250 255  
Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala  
260 265 270  
Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu  
275 280 285

Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln  
 290 295 300

Glu Gln Gln  
 305

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	1	5	10	15
Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	20	25	30	
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	35	40	45	
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	50	55	60	
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	65	70	75	80
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	85	90	95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	100	105	110	
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	115	120	125	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	130	135	140	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	145	150	155	160
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	165	170	175	
Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	180	185	190	
Ser	Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	195	200	205	

Leu Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp  
 210 215 220  
 Glu Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu  
 225 230 235 240  
 Glu Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile  
 245 250 255  
 Glu Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala  
 260 265 270  
 Ala Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu  
 275 280 285  
 Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln  
 290 295 300  
 Glu Gln Gln  
 305

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu  
 1 5 10 15  
 Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala  
 20 25 30  
 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu  
 35 40 45  
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser  
 50 55 60  
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu  
 65 70 75 80  
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly  
 85 90 95  
 Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val  
 100 105 110  
 Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met  
 115 120 125  
 Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser

130	135	140
Ala Phe Gln Arg Arg	Ala Gly Gly Val Leu	Val Ala Ser His Leu Gln
145	150	155 160
Ser Phe Leu Glu Val	Ser Tyr Arg Val Leu	Arg His Leu Ala Gln Pro
	165	170 175
Tyr Val Pro Gln Pro	Pro Val Asn Ala Gly	Gly Gly Gly Ser Gly Gly Gly
	180	185 190
Ser Gly Gly Gly Ser	Glu Gly Gly Gly Ser	Glu Gly Gly Gly Ser Glu
	195	200 205
Gly Gly Gly Ser Glu	Gly Gly Gly Ser Gly	Gly Gly Ser Gly Ser Gly
	210	215 220
Asp Phe Asp Tyr Glu	Asn Met Ala Asn Cys	Ser Ile Met Ile Asp Glu
225	230	235 240
Ile Ile His His Leu	Lys Arg Pro Pro Ala	Pro Leu Leu Asp Pro Asn
	245	250 255
Asn Leu Asn Asp Glu	Asp Val Ser Ile Leu	Met Asp Arg Asn Leu Arg
	260	265 270
Leu Val Arg Ala Val	Lys Asn Leu Glu Asn	Ala Ser Gly Ile Glu Ala
	275	280 285
Ile Leu Arg Asn Leu	Gln Pro Cys Leu Pro	Ser Ala Thr Ala Ala Pro
	290	295 300
Ser Arg His Pro Ile	Ile Ile Lys Ala Gly	Asp Trp Gln Glu Phe Arg
305	310	315 320
Glu Lys Leu Thr Phe	Tyr Leu Val Thr Leu	Glu Gln Ala Gln Glu Gln
	325	330 335
Gln		

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
1 5 10 15
Leu Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala
20 25 30



(A) LENGTH: 322 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	1	5	10	15
Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	20	25	30	
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	35	40	45	
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	50	55	60	
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu	65	70	75	80
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	85	90	95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	100	105	110	
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	115	120	125	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	130	135	140	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	145	150	155	160
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	165	170	175	
Tyr	Val	Ile	Glu	Gly	Arg	Ile	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	180	185	190	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	195	200	205	
Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	210	215	220	
Lys	Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	225	230	235	240
Asp	Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	245	250	255	
Ala	Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu				

260	265	270
Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala		
275	280	285
Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe		
290	295	300
Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu		
305	310	315
		320
Gln Gln		

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu
1				5					10					15	
Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala
		20						25					30		
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu
		35					40					45			
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser
	50					55					60				
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu
65				70					75					80	
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly
			85					90						95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val
		100						105					110		
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met
		115					120					125			
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
	130					135					140				
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
145				150					155					160	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
				165					170					175	

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly  
 180 185 190  
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser  
 195 200 205  
 Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly  
 210 215 220  
 Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn Met Ala Asn Cys  
 225 230 235 240  
 Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn  
 245 250 255  
 Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu  
 260 265 270  
 Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala  
 275 280 285  
 Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn  
 290 295 300  
 Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro  
 305 310 315 320  
 Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr  
 325 330 335  
 Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln  
 340 345

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
 1 5 10 15  
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
 20 25 30  
 Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
 35 40 45  
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
 50 55 60



Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
 65 70 75 80  
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
 85 90 95  
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
 100 105 110  
 Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly  
 115 120 125  
 Gly Ser Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln  
 130 135 140  
 Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp  
 145 150 155 160  
 Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His  
 165 170 175  
 Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala  
 180 185 190  
 Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu  
 195 200 205  
 Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala  
 210 215 220  
 Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln  
 225 230 235 240  
 Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu  
 245 250 255  
 Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala  
 260 265 270  
 Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser  
 275 280 285  
 His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu  
 290 295 300  
 Ala Gln Pro  
 305

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	115	120	125	
Gly	Ser	Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	130	135	140	
His	Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	145	150	155	160
Asp	Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	165	170	175	
Leu	Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	180	185	190	
Ile	Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	195	200	205	
Ala	Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	210	215	220	
Glu	Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	225	230	235	240
Gln	Glu	Gln	Gln																

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15  
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp  
20 25 30  
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser  
35 40 45  
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60  
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80  
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95  
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110  
Gln Tyr Val Ile Glu Gly Gly Gly Ser Pro Gly Glu Pro Ser Gly Pro  
115 120 125  
Ile Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser  
130 135 140  
Pro Asn Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser  
145 150 155 160  
Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly  
165 170 175  
Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro  
180 185 190  
Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro  
195 200 205  
Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
210 215 220  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu  
225 230 235 240  
Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu  
245 250 255  
Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu  
260 265 270  
Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe  
275 280 285  
Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His  
290 295 300

Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala  
 305 310 315 320

Gln Pro

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	85	90	95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	100	105	110	
Gln	Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	115	120	125	
Ile	Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	130	135	140	
Pro	Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	145	150	155	160
Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	165	170	175	
Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	180	185	190	
Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	195	200	205	
Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala				

210	215	220
Ala Pro Ser Arg His	Pro Ile Ile Ile Lys	Ala Gly Asp Trp Gln Glu
225	230	235 240
Phe Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln		
	245	250 255
Glu Gln Gln		

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu
1				5					10					15	
Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala
			20					25					30		
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu
		35					40					45			
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser
	50					55					60				
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gly	Leu
65				70						75				80	
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly
			85						90					95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val
			100					105					110		
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met
		115					120					125			
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
		130				135					140				
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
145					150					155				160	
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
				165					170					175	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
			180					185					190		

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro  
 195 200 205  
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu  
 210 215 220  
 Lys Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu  
 225 230 235 240  
 Asp Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu  
 245 250 255  
 Ser Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu  
 260 265 270  
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala  
 275 280 285  
 Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe  
 290 295 300  
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu  
 305 310 315 320  
 Gln Gln

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu  
 1 5 10 15  
 Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala  
 20 25 30  
 Leu Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu  
 35 40 45  
 Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser  
 50 55 60  
 Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gly Leu  
 65 70 75 80  
 His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly  
 85 90 95

Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	100	105	110	
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	115	120	125	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	130	135	140	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	145	150	155	160
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	165	170	175	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile	180	185	190	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro	195	200	205	
Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	210	215	220	
Lys	Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	225	230	235	240
Asp	Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	245	250	255	
Ser	Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	260	265	270	
Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	275	280	285	
Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	290	295	300	
Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	305	310	315	320
Gln	Gln																		

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Ala Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu

1	5	10	15
Leu Lys Cys	Leu Glu Gln Val Arg	Lys Ile Gln Gly Asp	Gly Ala Ala
20	25	30	
Leu Gln Glu	Lys Leu Cys Ala Thr Tyr	Lys Leu Cys His	Pro Glu Glu
35	40	45	
Leu Val Leu	Leu Gly His Ser Leu Gly	Ile Pro Trp Ala	Pro Leu Ser
50	55	60	
Ser Cys Pro	Ser Gln Ala Leu Gln Leu Ala	Gly Cys Leu Ser	Gly Leu
65	70	75	80
His Ser Gly	Leu Phe Leu Tyr Gln Gly	Leu Leu Gln Ala	Leu Glu Gly
	85	90	95
Ile Ser Pro	Glu Leu Gly Pro Thr Leu Asp	Thr Leu Gln Leu	Asp Val
	100	105	110
Ala Asp Phe	Ala Thr Thr Ile Trp Gln Gln	Met Glu Glu Leu	Gly Met
	115	120	125
Ala Pro Ala	Leu Gln Pro Thr Gln Gly Ala	Met Pro Ala Phe	Ala Ser
	130	135	140
Ala Phe Gln	Arg Arg Ala Gly Gly Val Leu	Val Ala Ser His	Leu Gln
145	150	155	160
Ser Phe Leu	Glu Val Ser Tyr Arg Val Leu	Arg His Leu Ala	Gln Pro
	165	170	175
Tyr Val Glu	Gly Gly Gly Gly Ser Pro Gly	Gly Gly Gly Ser	Gly Gly Gly
	180	185	190
Ser Asn Met	Ala Asn Cys Ser Ile Met Ile	Asp Glu Ile Ile	His His
	195	200	205
Leu Lys Arg	Pro Pro Ala Pro Leu Leu Asp	Pro Asn Asn Leu	Asn Asp
	210	215	220
Glu Asp Val	Ser Ile Leu Met Asp Arg Asn	Leu Arg Leu Pro	Asn Leu
225	230	235	240
Glu Ser Phe	Val Arg Ala Val Lys Asn Leu	Glu Asn Ala Ser	Gly Ile
	245	250	255
Glu Ala Ile	Leu Arg Asn Leu Gln Pro Cys	Leu Pro Ser Ala	Thr Ala
	260	265	270
Ala Pro Ser	Arg His Pro Ile Ile Ile Lys	Ala Gly Asp Trp	Gln Glu
	275	280	285
Phe Arg Glu	Lys Leu Thr Phe Tyr Leu Val	Thr Leu Glu Gln	Ala Gln
	290	295	300
Glu Gln Gln			
305			

(2) INFORMATION FOR SEQ ID NO:159:



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 307 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	1	5	10	15
Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	20	25	30	
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	35	40	45	
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser	50	55	60	
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gly	Leu	65	70	75	80
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly	85	90	95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	100	105	110	
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met	115	120	125	
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	130	135	140	
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	145	150	155	160
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	165	170	175	
Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly	180	185	190	
Ser	Asn	Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	195	200	205	
Leu	Lys	Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	210	215	220	
Glu	Asp	Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	225	230	235	240
Glu	Ser	Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	245	250	255	

Glu	Ala	Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala
			260					265					270		
Ala	Pro	Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu
		275					280					285			
Phe	Arg	Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln
	290					295					300				
Glu	Gln	Gln													
305															

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met	Ala	Pro	Ala	Arg	Ser	Pro	Ser	Pro	Ser	Thr	Gln	Pro	Trp	Glu	His
1				5					10					15	
Val	Asn	Ala	Ile	Gln	Glu	Ala	Arg	Arg	Leu	Leu	Asn	Leu	Ser	Arg	Asp
		20					25						30		
Thr	Ala	Ala	Glu	Met	Asn	Glu	Thr	Val	Glu	Val	Ile	Ser	Glu	Met	Phe
		35					40					45			
Asp	Leu	Gln	Glu	Pro	Thr	Cys	Leu	Gln	Thr	Arg	Leu	Glu	Leu	Tyr	Lys
	50					55					60				
Gln	Gly	Leu	Arg	Gly	Ser	Leu	Thr	Lys	Leu	Lys	Gly	Pro	Leu	Thr	Met
65					70					75					80
Met	Ala	Ser	His	Tyr	Lys	Gln	His	Cys	Pro	Pro	Thr	Pro	Glu	Thr	Ser
			85						90					95	
Cys	Ala	Thr	Gln	Ile	Ile	Thr	Phe	Glu	Ser	Phe	Lys	Glu	Asn	Leu	Lys
			100					105					110		
Asp	Phe	Leu	Leu	Val	Ile	Pro	Phe	Asp	Cys	Trp	Glu	Pro	Val	Gln	Glu
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu
1				5					10					15	
Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala
			20					25					30		
Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu
			35				40					45			
Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	Ser
	50					55					60				
Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	Gln	Leu
65					70					75					80
His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Glu	Gly
				85					90					95	
Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val
			100					105					110		
Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	Glu	Glu	Leu	Gly	Met
			115				120					125			
Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser
	130					135					140				
Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln
145					150					155					160
Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met	Ala	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu
1				5					10					15	
Leu	Lys	Ser	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala
			20					25					30		

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

## 172

Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu  
 100 105 110  
 Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu  
 115 120 125  
 Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr  
 130 135 140  
 Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu  
 145 150 155 160  
 Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu  
 165 170 175  
 Gln Ser Ser Leu Arg Ala Leu Arg Gln Met  
 180 185

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
 1 5 10 15  
 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro  
 20 25 30  
 Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe  
 35 40 45  
 Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp  
 50 55 60  
 Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg  
 65 70 75 80  
 Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser  
 85 90 95  
 Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr  
 100 105 110  
 Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala  
 115 120 125  
 Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu  
 130 135 140  
 Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg

145

150

155

## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110

Gln Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly
          115          120          125

Gly Ser Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val
          130          135          140

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser
145          150          155          160

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala
          165          170          175

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys
          180          185          190

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met
          195          200          205

Ala Ala Arg Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly
          210          215          220

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu
225          230          235          240

```

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
245 250 255

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
260 265 270

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg  
275 280 285

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys  
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp  
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala  
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala  
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro  
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg  
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln  
100 105 110

Gln Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly  
115 120 125

Gly Ser Asn Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val  
130 135 140

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
145 150 155 160

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
165 170 175

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
180 185 190

Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
		195					200					205			
Ala	Ala	Arg	Gln	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly
	210					215					220				
Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu
225					230					235					240
Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp
				245					250					255	
Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val
			260					265					270		
Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg		
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met	Ala	Ser	Pro	Ala	Pro	Pro	Ala	Cys	Asp	Leu	Arg	Val	Leu	Ser	Lys
1				5					10					15	
Leu	Leu	Arg	Asp	Ser	His	Val	Leu	His	Ser	Arg	Leu	Ser	Gln	Cys	Pro
		20						25					30		
Glu	Val	His	Pro	Leu	Pro	Thr	Pro	Val	Leu	Leu	Pro	Ala	Val	Asp	Phe
		35					40					45			
Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp
	50					55					60				
Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg
65					70					75					80
Gln	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser
				85					90					95	
Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr
			100					105						110	
Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala
		115					120					125			
Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu
		130				135					140				
Met	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Tyr	Val	Ile	Glu	Gly



145		150		155		160
Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser Asn Met Ala Asn						
	165			170		175
Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro						
	180		185		190	
Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile						
	195		200		205	
Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg						
	210		215		220	
Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg						
	225		230		235	240
Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His						
		245		250		255
Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu						
	260		265		270	
Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln						
	275		280		285	

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ala Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys																			
1				5				10						15					
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro																			
			20					25						30					
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe																			
			35				40						45						
Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp																			
			50				55					60							
Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg																			
65						70				75									80
Gln Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser																			
						85			90										95
Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr																			
			100					105											110

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala  
 115 120 125  
 Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu  
 130 135 140  
 Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Glu Phe His Ala Tyr  
 145 150 155 160  
 Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly Ser  
 165 170 175  
 Asn Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu  
 180 185 190  
 Lys Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu  
 195 200 205  
 Asp Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu  
 210 215 220  
 Ala Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu  
 225 230 235 240  
 Ala Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala  
 245 250 255  
 Pro Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe  
 260 265 270  
 Arg Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu  
 275 280 285  
 Gln Gln  
 290

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACGTCCATGG CNTCNCNGC NCCNCCTGCT TGTGACCTCC GAGTC

45

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

AATAGCTGAA TTCTTACCCT TCCTGAGACA GATT

34

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TGACAAGCTT ACCTGACGCA GAGGGTGGAC CCT

33

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

ATGCACGAAT TCCCTGACGC AGAGGGTGGGA

30

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

AATTCCATGC ATAC

14

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTACGTATG

10

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

ATGGCTCCAG TACCACCAGG TGAAGATTCC AAAGATGTGG CCGCCCCACA CAGACAGCCA	60
CTCACCTCTT CAGAACGAAT TGACAAACAA ATTCGGTACA TCCTCGACGG GATATCAGCC	120
CTGAGAAAGG AGACATGTAA CAAGAGTAAC ATGTGTGAAA GCAGCAAAGA GCGCTAGCA	180
GAAAACAACC TGAACCTTCC AAAGATGGCT GAAAAAGATG GATGCTTCCA ATCCGGATTC	240
AATGAGGAGA CTTGCCTGGT GAAAATCATC ACTGGTCTTT TGGAGTTTGA GGTATACCTC	300
GAGTACCTCC AGAACAGATT TGAGAGTAGT GAGGAACAAG CCAGAGCTGT GCAGATGTCG	360
ACAAAAGTCC TGATCCAGTT CCTGCAGAAA AAGGCAAAGA ATCTAGATGC AATAACCACC	420
CCTGACCCAA CCACAAATGC ATCCCTGCTG ACGAAGCTGC AGGCACAGAA CCAGTGGCTG	480
CAGGACATGA CAACTCATCT CATTCTGCGC AGCTTTAAGG AGTTCCTGCA GTCCAGCCTG	540
AGGGCTCTTC GGCAAATGTA G	561

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ATGGCACC GG CTCGTTCCCC GTCCCCGTCT ACCCAGCCGT GGGAACACGT GAATGCCATC	60
CAGGAGGCCC GGCCTCTCCT GAACCTGAGT AGAGACACTG CTGCTGAGAT GAATGAAACA	120
GTAGAAGTGA TATCAGAAAT GTTTGACCTC CAGGAGCCGA CTTGCCTACA GACCCGCCTG	180
GAGCTGTACA AGCAGGGCCT GCGGGGCAGC CTCACCAAGC TCAAGGGCCC CTTGACCATG	240
ATGGCCAGCC ACTACAAGCA GCACTGCCCT CCAACCCCGG AAATTTCCTG TGCAACCCAG	300
ATTATCACCT TTGAAAGTTT CAAAGAGAAC CTGAAGGACT TCCTGCTTGT CATCCCCTTT	360
GACTGCTGGG AGCCAGTCCA GGAGTGATAA GGATCCGAAT TC	402

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ATGGCTACAC CATTAGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA	60
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC	120
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG	180
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC	240
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCC TGAAGGGAT ATCCCCGAG	300
TTGGGTCCCA CTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG	360
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC	540
GAATTC	546

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCTACAC CATTAGGACC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTGCTTA 60  
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC 120  
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG 180  
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC 240  
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG 300  
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG 360  
CAGCAGATGG AAGAACTGGG AATGGCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG 420  
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG 480  
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC 540  
GAATTC 546

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTACAC CATTGGGCCC TGCCAGCTCC CTGCCCCAGA GCTTCCTGCT CAAGTCTTTA 60  
GAGCAAGTGA GGAAGATCCA GGGCGATGGC GCAGCGCTCC AGGAGAAGCT GTGTGCCACC 120  
TACAAGCTGT GCCACCCCGA GGAGCTGGTG CTGCTCGGAC ACTCTCTGGG CATCCCCTGG 180  
GCTCCCCTGA GCTCCTGCCC CAGCCAGGCC CTGCAGCTGG CAGGCTGCTT GAGCCAACTC 240  
CATAGCGGCC TTTTCCTCTA CCAGGGGCTC CTGCAGGCCC TGGAAGGGAT ATCCCCGAG 300  
TTGGGTCCCA CCTTGGACAC ACTGCAGCTG GACGTCGCCG ACTTTGCCAC CACCATCTGG 360

CAGCAGATGG AAGAACTGGG AATGGCCCCCT GCCCTGCAGC CCACCCAGGG TGCCATGCCG	420
GCCTTCGCCT CTGCTTTCCA GCGCCGGGCA GGAGGGGTCC TGGTTGCTAG CCATCTGCAG	480
AGCTTCCTGG AGGTGTCGTA CCGCGTTCTA CGCCACCTTG CGCAGCCCTG ATAAGGATCC	540
GAATTC	546

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	420
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGG	465

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCTGTCAACC CGGGCGGCGG CTCTGGTGGT GGTTCCTGGT GCGGCTCTGA GGGTGGCGGC	60
TCTGAGGGTG GCGGTTCTGA GGGTGGCGGC TCTGAGGGTG GCGGTTCCGG TGGCGGCTCC	120
GGTTCCGGTA ACATGTATTA TGA	143

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ATCGTCTGAC CTCCCGGGCC TCCTGTCAAT GCTGGCGGCG GCTCTGGTGG TGGTTCTGGT	60
GGCGGCTCTG AGGGTGGCGG CTCTGAGGGT GGCGGTTCTG AGGGTGGCGG CTCTGAGGGT	120
GGCGGTTCCG GTGGCGGCTC CGGTTCCGGT GATTTTGATT ATGAAAACAT GTCAAACGCT	180

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAATCGA GGGAAGGATT	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGCGCC GCCTGCTTGT	420
GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCATG TCCTTCACAG CAGACTGAGC	480
CAGTGCCCAG AGGTTACCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGACTTTAGC	540
TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG	600
ACCCTTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA	660
TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC	720



CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC	780
TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG	840
TCCACCCTCT GCGTCAGG	858

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAAGTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAGT ACGTAGAGGG CGGTGGAGGC	360
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCGT CTCCGGCGCC GCCTGCTTGT	420
GACCTCCGAG TCCTCAGTAA ACTGCTTCGT GACTCCCATG TCCTTCACAG CAGACTGAGC	480
CAGTGCCAG AGGTTACCCC TTTGCCTACA CCTGTCCTGC TGCCTGCTGT GGAAGTTAGC	540
TTGGGAGAAT GGAAAACCCA GATGGAGGAG ACCAAGGCAC AGGACATTCT GGGAGCAGTG	600
ACCCTTCTGC TGGAGGGAGT GATGGCAGCA CGGGGACAAC TGGGACCCAC TTGCCTCTCA	660
TCCCTCCTGG GGCAGCTTTC TGGACAGGTC CGTCTCCTCC TTGGGGCCCT GCAGAGCCTC	720
CTTGGAACCC AGCTTCCTCC ACAGGGCAGG ACCACAGCTC ACAAGGATCC CAATGCCATC	780
TTCCTGAGCT TCCAACACCT GCTCCGAGGA AAGGTGCGTT TCCTGATGCT TGTAGGAGGG	840
TCCACCCTCT GCGTCAGG	858

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACCTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360
ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG	420
GTGCGTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGATCGA GGAAGGATT	480
TCCCCGGGTG GTGGTTCTGG CGGCGGCTCC AACATGGCTA ACTGCTCTAT AATGATCGAT	540
GAAATTATAC ATCACTTAAA GAGACCACCT AACCTTTTGC TGGACCCGAA CAACCTCAAT	600
TCTGAAGACA TGGATATCCT GATGGAACGA AACCTTCGAA CTCCAAACCT GCTCGCATTC	660
GTAAGGGCTG TCAAGCACTT AGAAAATGCA TCAGGTATTG AGGCAATTCT TCGTAATCTC	720
CAACCATGTC TGCCCTCTGC CACGGCCGCA CCCTCTCGAC ATCCAATCAT CATCAAGGCA	780
GGTGACTGGC AAGAATTCCG GGAAAACTG ACGTTCTATC TGGTTACCCT TGAGCAAGCG	840
CAGGAACAAC AG	852

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

ATGGCGTCTC CGGCGCCGCC TGCTTGTGAC CTCCGAGTCC TCAGTAAACT GCTTCGTGAC	60
TCCCATGTCC TTCACAGCAG ACTGAGCCAG TGCCCAGAGG TTCACCCTTT GCCTACACCT	120
GTCCTGCTGC CTGCTGTGGA CTTTAGCTTG GGAGAATGGA AAACCCAGAT GGAGGAGACC	180
AAGGCACAGG ACATTCTGGG AGCAGTGACC CTTCTGCTGG AGGGAGTGAT GGCAGCACGG	240
GGACAACCTGG GACCCACTTG CCTCTCATCC CTCCTGGGGC AGCTTTCTGG ACAGGTCCGT	300
CTCCTCCTTG GGGCCCTGCA GAGCCTCCTT GGAACCCAGC TTCCTCCACA GGGCAGGACC	360

ACAGCTCACA AGGATCCCAA TGCCATCTTC CTGAGCTTCC AACACCTGCT CCGAGGAAAG 420  
 GTGCGTTTTCC TGATGCTTGT AGGAGGGTCC ACCCTCTGCG TCAGGGAATT CCATGCATAC 480  
 GTAGAGGGCG GTGGAGGCTC CCCGGGTGGT GGTTCCTGGCG GCGGCTCCAA CATGGCTAAC 540  
 TGCTCTATAA TGATCGATGA AATTATACAT CACTTAAAGA GACCACCTAA CCCTTTGCTG 600  
 GACCCGAACA ACCTCAATTC TGAAGACATG GATATCCTGA TGGAACGAAA CCTTCGAACT 660  
 CCAAACCTGC TCGCATTCGT AAGGGCTGTC AAGCACTTAG AAAATGCATC AGGTATTGAG 720  
 GCAATTCCTC GTAATCTCCA ACCATGTCTG CCCTCTGCCA CGGCCGCACC CTCTCGACAT 780  
 CCAATCATCA TCAAGGCAGG TGACTGGCAA GAATTCCGGG AAAAAGTGAC GTTCTATCTG 840  
 GTTACCCTTG AGCAAGCGCA GGAACAACAG 870

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Ser Arg Leu Pro Val Leu Leu Leu Leu Gln Leu Leu Val Arg Pro  
 1 5 10 15

Ala Met

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly  
 1 5 10 15

Ser Asn

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Tyr Val Ile Glu Gly Lys Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly  
1                  5                  10                  15

Ser Asn

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Tyr Val Glu Gly Gly Gly Gly Ser Pro Gly Gly Gly Ser Gly Gly Gly  
1                  5                  10                  15

Ser Asn

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Glu Pro Ser Gly Pro Ile  
1                  5                  10                  15

Ser Thr Ile Asn Pro Ser Pro Pro Ser Lys Glu Ser His Lys Ser Pro

Asn

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Tyr	Val	Ile	Glu	Gly	Lys	Ile	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
1				5					10					15	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
			20					25					30		

Asn

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Tyr	Val	Glu	Gly	Gly	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Ser	Gly	Pro	Ile
1				5					10					15	
Ser	Thr	Ile	Asn	Pro	Ser	Pro	Pro	Ser	Lys	Glu	Ser	His	Lys	Ser	Pro
			20					25					30		

Asn

(2) INFORMATION FOR SEQ ID NO:194:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gly Gly Gly Ser Gly Gly Gly  
1 5 10 15  
Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu  
20 25 30  
Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly  
35 40 45

Asn

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Tyr Val Ile Glu Gly Arg Ile Ser Pro Gln Pro Pro Val Asn Ala Gly  
1 5 10 15  
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser  
20 25 30  
Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly  
35 40 45  
Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Asn  
50 55 60

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

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